```
ACACCATTTG TCTTCATGTA ACCCCATTAG CTATACCCTC TAGTGCAAGG AAACCATAGG
        10         20         30         40         50         60

GCCTAGGTCA CACCATGAGG CTGCNCTTAC AAGTTATGCA AAAACTATGG ACTTGGGAGA
        70         80         90        100        110        120

CCTGTGCGTA ACAACATCAC ACNCCAAATT TAACCAGCTC TCCCCATAAC AGCACGCTCA
       130        140        150        160        170        180

TGTGTTACTG AGGAAATGCC TGTGGATTGG AGTGTGTTCT GTGTGCAGGA GGCTGGTCCA
       190        200        210        220        230        240

GGTTTCACTT CTGCAGGACA CTGGACGTTT CCCAAAACCA GCAGACTTTC CCCACGTGCA
       250        260        270        280        290        300

CACACACCCC TTCTCATTTT GCCTCTACAT CCATATCCAC TGGGCCCTTC AGGCACCTAC
       310        320        330        340        350        360

TAATGCCCTA GAACCTAAAA CCATCATCTG GGGCCCAGTT CCCTGAATGG CCCTAATCTC
       370        380        390        400        410        420

TTCCTCTGCT GGAATGAGTC CAGTGCCCAC TTCCTCCAAC GGTGAAATTG CTGGGCTGCT
       430        440        450        460        470        480

ACAGATCAGG AACTCACTGC TTCCTCATAG GGGCAGCCGA CTTCACTGCT CTGCAACAGC
       490        500        510        520        530        540

GACCACCCCT AGCGAGGCTT GAGATGCCTC TTGCCTCCTT AAGACTGAGG GAGACGCTTC
       550        560        570        580        590        600

AGCTCTCACT CCACTGCCCC AAGTCCTCCA CAGCGCGGTG CCTGCTGCCT TCACACAGAG
       610        620        630        640        650        660

CTGCAGGGGN AGGTCCTGTG TATCCGGCCT GCTGGACCAG CGCTGTGCAC AACCCTCCCA
       670        680        690        700        710        720

TGGCAACAGT GGCTGCCCGG CCTGCACACT GGGCTTGGCA ACCTCGCTGT AGGTATTTAT
       730        740        750        760        770        780

TCCCTCAGGA GTGACTGCAT TCTTTTCCCA TTTCCAGAAA ACTGATGCCA TTTACCTCAC
       790        800        810        820        830        840

TATGAGGAGG AGGAGGAGGA GGAGGGTGGA GAGTGGTACA TTTTAAAATG TGCACTATTC
       850        860        870        880        890        900

TCCCTAGGAC TCCCCCTCAA ATAACCCAGG AGGGACCATA CCAGCTCATT CCTGTGTATC
       910        920        930        940        950        960

CCAAGCATAN GAGTAATCAT CCCACTCATG CTGAGTGTAT GGTGGCCATT AAGCCTGCCC
       970        980        990       1000       1010       1020
```

Figure 1

```
TGAACTGGCT TTAGAACAAG GTGTTTGAGC ACACAGCACC GTCTTGCTGC CACCTTGGCC
      1030        1040        1050        1060        1070        1080

CCCTCCCTTG TGAGACCTCT GAGACACATT NAGGTCTCAC CTAAAAATCT CAGGATTTCT
      1090        1100        1110        1120        1130        1140
AGGCCCAAAN CGGTCCTAAA AAATTGTTCA GTCTGAACTC TCTAAGGTCA AGAGAAGAGG
      1150        1160        1170        1180        1190        1200

TGGTTGCTCC CTCTAAGAAA CCACATGTTG CATGTACATC CTTAATTCCG GAAAGTCCAA
      1210        1220        1230        1240        1250        1260

CAAACCTGCC CTGCTTAGCA ACACAAGCCG AGGTGGTACT CCTCTCACCC GGGCATTCTC
      1270        1280        1290        1300        1310        1320

CAACACACCT GTTTGTCCAA ACAGCTTTGA TTTGTTTTTA TAGTTGGACC CCAGGTTCCC
      1330        1340        1350        1360        1370        1380

AGGAGGCTGG TTCAGGCCAT ATTCCAAATC CTCATCTGTG TGTGAGTGGC ATTCTTAGCC
      1390        1400        1410        1420        1430        1440

TAGCCTCCTT ACAGGGTGGA TACTATGATA CACAGCCAGG CTGTCCCAGT GGCTTTCAAT
      1450        1460        1470        1480        1490        1500

ATTCTTTTGG TCCAGATAGT TCAGCCTCAG CACCPGTGTA GGCATCACAG GGTCAATTGT
      1510        1520        1530        1540        1550        1560

CTTAGGAGTC ATGGAGAATT CATAGTTGGT AGCTACCTGG GCCTGGCCAG GGCTGACCAT
      1570        1580        1590        1600        1610        1620

AGACAAGGCA TCCCTCTGTG AACTCCTATT TTAATGCCAG CTTCCCAACA AATTTCTCAA
      1630        1640        1650        1660        1670        1680
                                    CAAT box
                                    ----
CTGCTCTTAC CAGCAGGTAT TTAAACTACT CAATAGAAAG TAACCCTGAA AATTAGGACA
      1690        1700        1710        1720        1730        1740
                  TATA box
                  ----------
CCTGTTCCCA AAAGACCCTT AAATAGGGGA AGTCCTTTCN CTGCTTGTGC ACAGCTGCTG
      1750        1760        1770        1780        1790        1800
                                          |->mRNA --------------------
ATGTGGCAAC ATGAGGCCTG GGACAGGGGA CTGTCCTCTG CCCACTCTGG TAGCCTCACG
      1810        1820        1830        1840        1850        1860
                Spsite
-- exon 1 ---->######
TAGCTTAACA ATCTGTCAGT AATACAATAC AAAACTTAAA CTTTCATACT GCGGTTCCAC
      1870        1880        1890        1900        1910        1920
                                                  ->
CCAGGAAGCT GTGTTCCCAA TCTGACCCGT GATTATGGGG CCACCTCAGA GGGNACCCAG
      1930        1940        1950        1960        1970        1980
```


Figure 1(continued)

```
TGAGGGAATA TTTTGCCATC TGGGACTGTT GGTTGCTGGG GGCAGTGGCT ATGAGCTCAG
      1990       2000       2010       2020       2030       2040

TTAATAAACT CAAGCAGTTT CCTTCCAAAC ACACATGTCC TACTTAACGT GTCCAACAGA
      2050       2060       2070       2080       2090       2100

                                                            ------
GATGATCATA CTCATANGCT GCTAAAACAT TANTTTTATT TTGAGAAAAG TCTATTCATG
      2110       2120       2130       2140       2150       2160
--------------------- Alu insert ---------------------------------
TTCTTGGCCC ATGGAGTTTT CATTTNATTA NTTTATTTAT TTTGCAGAGA TGGAGTCTCA
      2170       2180       2190       2200       2210       2220

-----------------------------------------------------------------
CTATGTTGCT CAAGCTGGTC TCCAACTCCT GGGCTCAAGC GATCTTCCTA CTTTGGCCTT
      2230       2240       2250       2260       2270       2280

-----------------------------------------------------------
TGAAAGCGCT GAGATTGCCT GTGTGAGCCA TCATGGGGGC TCACTGGCCC ACTGATTAAT
      2290       2300       2310       2320       2330       2340

CAGATTAATT GTTTTTTGCT ATTGAANTTG TTTGACTTCC TTGTATATTC GGATATTTAC
      2350       2360       2370       2380       2390       2400

CCATTCTAAC ACGTAGGGTT TGCAAATATT TTCTCTCATG TTCTGTGTTG CCTTTTCACT
      2410       2420       2430       2440       2450       2460

CAGTTGATGG TTTCCTTTGC TGTGCAGGTG CTTTAGTGTT CAACGCAGCC CCGCTTGTCT
      2470       2480       2490       2500       2510       2520

ATTTTCCATT TTATTGCCTG TCCCTTTGAT GTCATAGCCA AGAAATAATT GCCCAGATTA
      2530       2540       2550       2560       2570       2580

ATGTCAAAAA GCTTTATCCC TATATATTCT TCTAGTAGTT TATGGTTTCA GATCTTATGT
      2590       2600       2610       2620       2630       2640

TTAGGTCTTC AATCCATTGA GTTGATTTTT GTATGTGGTA TAAGAAAAAA GACCACATGT
      2650       2660       2670       2680       2690       2700

ATACATATCT CAAATTCTAA GGTAGTATAT ATTAGACACA TACAATGTGT CTATTTACAC
      2710       2720       2730       2740       2750       2760

ACATTGAGCT GAAAATAATA AACATATTTT TATCTTTCAA TCAACTCTAT CTCTATCTCA
      2770       2780       2790       2800       2810       2820

CTGAACTTGT TTCACCTATA GCCTGATGAG GTTGCTGTCC TCTCTACCCC AGCTCCTATA
      2830       2840       2850       2860       2870       2880

GGAGACTGCT CATCCCCTAA CCTCAAAAAC CCCTTCATGA GGGTGATAAT GCCCTTGAAT
      2890       2900       2910       2920       2930       2940
```

Figure 1(continued)

```
CCTGCAATGA ATTAGTTCTC TACTACAGTG GAATTCAGGT CTGTTATGAG GGTCTGGATC
      2950       2960       2970       2980       2990       3000

TCTGAAGAGA AGAGCTCTCA TTTTCAGAAA ATAAGCAGGA TTTATTCCCT GAAATTACTG
      3010       3020       3030       3040       3050       3060

AATTAAATCA CTGTTTCGAT TACTTTTTGC AATATTAAAA GTAAATATTT AAACAGGTAA
      3070       3080       3090       3100       3110       3120

AAACAGAAAT AATGGTAGGG TCCTTATCAT CACCGTGAAT TCCAAGCTAG CATAGACACT
      3130       3140       3150       3160       3170       3180

AAACCTAGAG ATTCACACTA GAATGAAAGC TGGGAGAGCA GAGGAGTCTC AGAAGGATGT
      3190       3200       3210       3220       3230       3240

GGAGGCCAAT GGACACCTGC AACCTCTCCA ACGAAATGCC TACCTCCTCT CACTGCAGCA
      3250       3260       3270       3280       3290       3300

TCCATCTCTG AGCCTTCTCG CAGCAGAGCT ATAAATTCAG CCTGGCTCCT CCGTTCCCAC
      3310       3320       3330       3340       3350       3360

                                  Spsite          CDS start
                                  ###<------------***------------
ACATCCACTC CTGCTCTCCC TCCTCTCCTC CAGGTGACTA CAGTTATGAG GACCCTCACC
      3370       3380       3390       3400       3410       3420

------------------------ Exon 2 -----------------------------
CTCCTCTCTG CCTTTCTCCT GGTGGCCCTT CAGGCCTGGG CAGAGCCGCT CCAGGCAAGA
      3430       3440       3450       3460       3470       3480

------------------------------------------------------------------
GCTCATGAGA TGCCAGCCCA GAAGCAGCCT CCAGCAGATG ACCAGGATGT GGTCATTTAC
      3490       3500       3510       3520       3530       3540

                                    Spsite
---------------------------------------->### ###
TTTTCAGGAG ATGACAGCTG CTCTCTTCAG GTTCCAGGTG AGAGATGCCA GCATGCAGAG
      3550       3560       3570       3580       3590       3600

CTACAGACTA GACAGAAGGA CAGGAGACAG GCTCTGGAAT TGGATCTCAG TGGCAGATGT
      3610       3620       3630       3640       3650       3660

CACTTAGGTG GCTATACTTA ACATCTCTGG TCCTGGATTT TCTCATATCT AAATGGAATA
      3670       3680       3690       3700       3710       3720

GAGAACCAAA GAAATCTAAG AGATTTTTCT TTCTCCAAAA ACTTGATTCC AAGATATGAC
      3730       3740       3750       3760       3770       3780

TGTGAAATTC ACTAGATTTA AGATATAAGG AGATGCTACC TAGTTCCTTC TGGAGCCAGA
      3790       3800       3810       3820       3830       3840
```


Figure 1(continued)

```
CAAACAAGCT TAAGTATATA GGAAAATATT TCACCCTGTC TATATAGGAG GTTTTAGAAC
      3850        3860        3870        3880        3890        3900

CTGGAGAGGA GCCTAAGAAT GTGTTCAGGT GTGTGTGTGA TGGGCAGGAA TGCAGAAAAG
      3910        3920        3930        3940        3950        3960

TGAAGCAAAG GAGAATGAGT CTCGAATCCT GTGTGACCAG CACTGCTCTG TGTATTTATT
      3970        3980        3990        4000        4010        4020

CCTATTGACT GAGATTGTTT GTGCTACCGG CTGTAATACA GCCAACATCA CTCATCAGCC
      4030        4040        4050        4060        4070        4080

AACATGTGAC TTCTCCAAGA TTCCCTTTAC CACCCACTGC TGNACCCCGT ACTCAGTTTC
      4090        4100        4110        4120        4130        4140

                          Spsite
                           ###<----------------------------------------
TGATGCTCTC TCTGGGTCCC CAGGCTCAAC AAAGGGCTTG ATCTGCCATT GCAGAGTACT
      4150        4160        4170        4180        4190        4200

---------------------------- Exon 3 -----------------------------
ATACTGCATT TTTGGAGAAC ATCTTGGTGG GACCTGCTTC ATCCTTGGTG AACGCTACCC
      4210        4220        4230        4240        4250        4260

              CDS stop
--------------***-------------------------------------------------
AATCTGCTGC TACTAAGCTT GCAGACTAGA GAAAAAGAGT TCATAATTTT CTTTGAGCAT
      4270        4280        4290        4300        4310        4320

                                                          Poly Ad
                                                           ******
-------------------------------------------------------------->
TAAAGGGAAT TGTTATTCTT ATACCTTGTC CTCGATTTCC TGTCCTCATC CCAAATAAAT
      4330        4340        4350        4360        4370        4380

ACTTGGTAAC ATGATTTCCG GGTTTTTTTT TTTTT
      4390        4400        4410
```


Figure 1(continued)

```
                10          20          30          40          50
DEF4   GGATCCCCATTTGTCTTCAGTGTAACCC-ATTAGTTAAACCGCCTACTGCAAGGAAACCA
       : :::::::::::::: :::::::: ::::: :: ::: ::: ::::::::::::::
DEFX     ACACCATTTGTCTTCA-TGTAACCCCATTAGCTATACCCTCTAGTGCAAGGAAACCA
                10          20          30          40          50

               60          70          80          90         100         110
DEF4   CAAGGCTTGGATCAGATCATGAGGCTGCCCT-ACAAGTTATGCCAAAAAATATGGACTTG
       : ::: : : ::: : ::::::::::::.:: :::::::::: ::::: ::::::::::
DEFX   TAGGGCCTAGGTCACACCATGAGGCTGCNCTTACAAGTTATGC-AAAAACTATGGACTTG
         60          70          80          90         100         110

              120         130         140         150         160         170
DEF4   GAAGACCTGTCTGTTATAATATCACAC-CCAAATCTAACCAGCTCTGCCAATAACAGCTC
       : ::::::::  :: : :: :::::: :::::: :::::::::: :: :::::::: :
DEFX   GGAGACCTGTGCGTAACAACATCACACNCCAAATTTAACCAGCTCTCCCCATAACAGCAC
         120         130         140         150         160         170

              180         190         200         210         220         230
DEF4   TCTCCTATGTTACTAGGAAAATGCCTATGGATTGGAGTGTGTTCTGTGTGCAGGAGGCTG
       ::: : :::::::  : :::::::: :::::::::::::::::::::::::::::::::
DEFX   GCTCATGTGTTACTGAGGAAATGCCTGTGGATTGGAGTGTGTTCTGTGTGCAGGAGGCTG
         180         190         200         210         220         230

              240         250         260         270         280         290
DEF4   GTCCAGGTTTCACTTCTGCAGGACACTGGACATC-CCCACAACCACCAGACCTTCCCCAC
       ::::::::::::::::::::::::::::::::: :  :::: ::::: ::::: :::::::::
DEFX   GTCCAGGTTTCACTTCTGCAGGACACTGGACGTTTCCCAAAACCAGCAGACTTTCCCCAC
         240         250         260         270         280         290

              300         310         320         330         340         350
DEF4   GTGCACACACACCCCTTCTCATTTTGCCTCTACATCCATATCCACTGGGCCCTTCAGGCA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DEFX   GTGCACACACACCCCTTCTCATTTTGCCTCTACATCCATATCCACTGGGCCCTTCAGGCA
         300         310         320         330         340         350

              360         370         380         390         400         410
DEF4   CCTACTAATGCCCTAGAACCTAAAACCATCATCTGGGGCCCAGTTCCCCAAATAGCCCTA
       :::::::::::::::::::::::::::::::::::::::::::::  ::: ::::::
DEFX   CCTACTAATGCCCTAGAACCTAAAACCATCATCTGGGGCCCAGTTCCCTGAATGGCCCTA
         360         370         380         390         400         410

              420         430         440         450         460         470
DEF4   ATTTCTTCCTCTGCTGGAATGAGTCCAGTGCCCACTTCCTCCAAAGGTGAAATTGCTGGG
       :: :::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DEFX   ATCTCTTCCTCTGCTGGAATGAGTCCAGTGCCCACTTCCTCCAACGGTGAAATTGCTGGG
         420         430         440         450         460         470

              480         490         500         510         520         530
DEF4   CCTGCAACAGATCAGGAACTCACTGCTTC-TCATAGGGGCAGCCGACTTCACTGCTCTGG
       : ::: :::::::::::::::::::::::: :::::::::::::::::::::::::::::
DEFX   C-TGCTACAGATCAGGAACTCACTGCTTCCTCATAGGGGCAGCCGACTTCACTGCTCTGC
         480         490         500         510         520         530
```


Figure 2

```
          540        550        560        570        580        590
DEF4  AACAGCGACCACCCCTAGCGAGGCTTGAGATGCCTCTTCCCTCCTTAAGACTGAGAGCGC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: : :
DEFX  AACAGCGACCACCCCTAGCGAGGCTTGAGATGCCTCTTGCCTCCTTAAGACTGAGGGAGA
         540        550        560        570        580        590

                              600        610        620        630
DEF4  CGCT-----------------GCCCCCAGTCCTCCATAGCCCAGTGCCTGGCTGCCTTCA
      ::::                 ::::: :::::::: ::: : ::::::: :::::::::
DEFX  CGCTTCAGCTCTCACTCCACTGCCCCAAGTCCTCCACAGCGCGGTGCCTG-CTGCCTTCA
         600        610        620        630        640        650

          640        650        660        670        680        690
DEF4  GCCAGAGCTGCAGGGG-AGGCCCTGAGCACCCAAGTCCTGCTGGACCAGCGCTGTGCACG
      ::::::::::::::: ::: :::: : : ::  : ::::::::::::::::::::::::
DEFX  CACAGAGCTGCAGGGGNAGGTCCTGTGTATCC--GGCCTGCTGGACCAGCGCTGTGCACA
         660        670        680        690        700        710

          700        710        720        730        740        750
DEF4  GCCCTCCCATGGCGGCAGGGGCTGCCTGGACTGCATACTGGGTTCAGCAACCTCACTATA
      ::::::::::::  ::: ::::::: :: ::::: :::::: :  :::::::: :: ::
DEFX  ACCCTCCCATGGCAACAGTGGCTGCCCGGCCTGCACACTGGGCTTGGCAACCTCGCTGTA
         720        730        740        750        760        770

          760        770        780        790        800        810
DEF4  GGTATTCATTCCCTCAGGAACAACTGCATTCTTTTCTCATTTCCAGAAACCTCATCCCGT
      :::::: ::::::::::::   :::::::::::::: :::::::::::: :: :: :: :
DEFX  GGTATTTATTCCCTCAGGAGTGACTGCATTCTTTTCCCATTTCCAGAAAACTGATGCCAT
         780        790        800        810        820        830

          820        830        840                   850        860
DEF4  TTACCTCACTACAAGGAGGAGGATG---------GTGGAGAGTGGTACATTTTAAAATGT
      :::::::::::  :::::::::: :          ::::::::::::::::::::::::::
DEFX  TTACCTCACTATGAGGAGGAGGAGGAGGAGGAGGGTGGAGAGTGGTACATTTTAAAATGT
         840        850        860        870        880        890

          870        880        890        900        910        920
DEF4  GCACTAGTCTCCCTGGGACTCCCCTTCAAATAACCCAGGAGGGACCACACAAGGGAAAGC
      :::::: ::::::: :::::::: :::::::::::::::::::::: :: ::   :  : :
DEFX  GCACTATTCTCCCTAGGACTCCCCCTCAAATAACCCAGGAGGGACCATACCAGCTCATTC
         900        910        920        930        940        950

          930        940        950        960        970        980
DEF4  TTATGCATCCCCCCCACCC-AGTGACCATCTTCCTAACTCTGGGTGTAGGGAGACTCGTA
      : :: :::::   ::  . ::: : ::::   :: :  ::: ::::: :: : :   ::
DEFX  CTGTGTATCCCAAGCATANGAGTAATCATCCCACTCATGCTGAGTGTATGGTGGCCATTA
         960        970        980        990       1000       1010

          990       1000       1010       1020       1030       1040
DEF4  AGCCTACG--GGATTGGTTTGGGAACAGGGTATTTGAGCTCACAACACAAGGTGATGCAA
      ::::: :   : : ::: ::  ::::: ::: :::::::: :::: :::
DEFX  AGCCTGCCCTGAACTGGCTTTAGAACAAGGTGTTTGAGCACACAGCACCG----------
         1020       1030       1040       1050       1060
```

Figure 2 (continued)

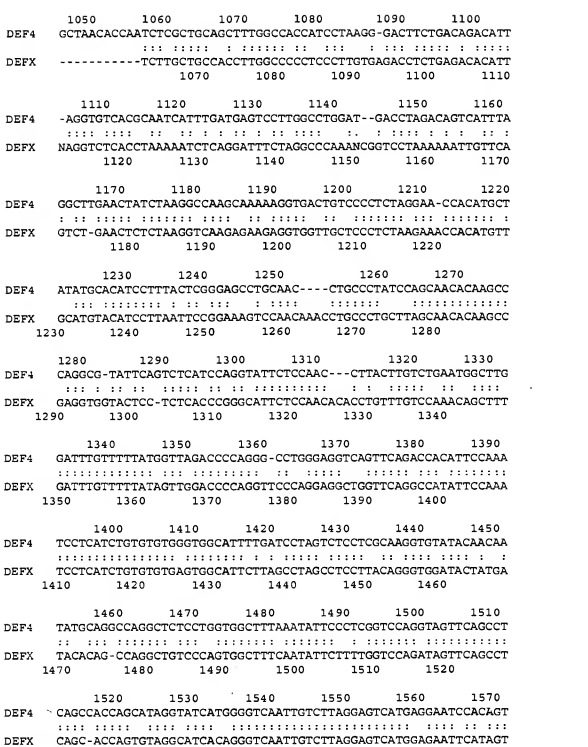

Figure 2(continued)

```
            1580       1590       1600       1610       1620       1630
DEF4    TGATTGCTGCCTGGGCCTGGCCAGGGCTGACCAAAGTAGACGAGGGGTCGGTACCTCCGT
        :: : ::: :::::::::::::::::::::::::::   ::::: :::  ::    :::: ::
DEFX    TGGTAGCTACCTGGGCCTGGCCAGGGCTGACCA---TAGACAAGGCATC----CCTCTGT
        1590       1600       1610          1620       1630

            1640       1650       1660       1670       1680       1690
DEF4    GGACTCCTGCTTGAACTCCAGCTTTCTGCCAAATTTCTCAACTGCCCTTGTTAACAGTTA
        : ::::::  :: ::  ::::::: :   ::::::::::::::::: :::   : ::: ::
DEFX    GAACTCCTATTTTAATGCCAGCTTCCCAACAAATTTCTCAACTGCTCTTACCAGCAGGTA
    1640       1650       1660       1670       1680       1690

                  CAAT box                                  -
            1700  ----1710       1720       1730       1740       1750
DEF4    TTTAAAGTACCCAATAGAAAGTAACGCTGAAAAATTAGGACACCTGATACCAAAAGACCC
        :::::: ::: ::::::::::::::: ::::::: :::::::::::: : ::::::::::
DEFX    TTTAAACTACTCAATAGAAAGTAACCCTGAAAA-TTAGGACACCTGTTCCCAAAAGACCC
    1700       1710       1720       1730       1740       1750

         TATA box
         ----------       1770       1780       1790       1800
DEF4    TTAAATAAGG-AAGTCCTCTC-CTCTGTGTGCATGGCTGCTCTTG---CTACATAAGACC
        :::::::: :: :::::::: :: ::   ::::::  ::::::   ::   : :::: :: ::
DEFX    TTAAATAGGGGAAGTCCTTTCNCTGCTTGTGCACAGCTGCTGATGTGGCAACATGAGGCC
    1760       1770       1780       1790       1800       1810

                              mRNA start -->                        SpSite
            1810       1820  |  1830       1840       1850       1860  ----
DEF4    TGGAACACAGGACTGCTGTCTGCCCTCTCTGCTCGCCCTGCCTAGCTTGAGGATCTGTAA
        ::: :::  :::::::   :::::::: ::::: : :::    : :::::: :  :::::: :
DEFX    TGGGACAGGGGACTGTCCTCTGCCCACTCTGGTAGCCTCACGTAGCTTAACAATCTGTCA
    1820       1830       1840       1850       1860       1870

            --              1880       1890       1900       1910       1920
DEF4    GTAACACAA-----AACTTAAACTTTCACATTGAGGTTTCAATATTGAAGCTGTGTCCCC
        :::: ::::      ::::::::::::::: : :: :::: ::      :::::::::: :::
DEFX    GTAATACAATACAAAACTTAAACTTTCATACTGCGGTTCCACCCAGGAAGCTGTGTTCCC
    1880       1890       1900       1910       1920       1930

            1930       1940       1950       1960       1970       1980
DEF4    AGTCTGACCTCTCACTGTGGGGCCACCCCAGAGGACCCAGCGTGAAGCCCCTGCTGTGAA
        : :::::::  : : : : :::::::::: :::::: . :   :::: :    :  : ::
DEFX    AATCTGACCCGTGATTATGGGGCCACCTCAGAGGGNACCCAGTGAGGGAA-TATTTTG--
    1940       1950       1960       1970       1980       1990

            1990       2000       2010       2020       2030       2040
DEF4    CTTCTATCTGGGTGTCTGGCGGCTGCTGGGGGTAATGGCTACTAGCTAAGTCAATAGAGA
        : :::::::   :::  :: :::::::::: : ::::::  :::: ::: ::::
DEFX    ---CCATCTGGGA--CTGTTGGTTGCTGGGGGCAGTGGCTATGAGCTCAGTTAATA----
           2000       2010       2020       2030       2040
```


Figure 2 (continued)

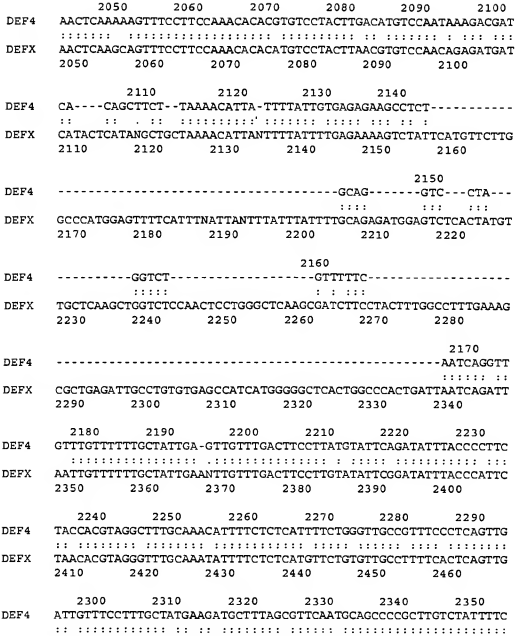

Figure 2(continued)

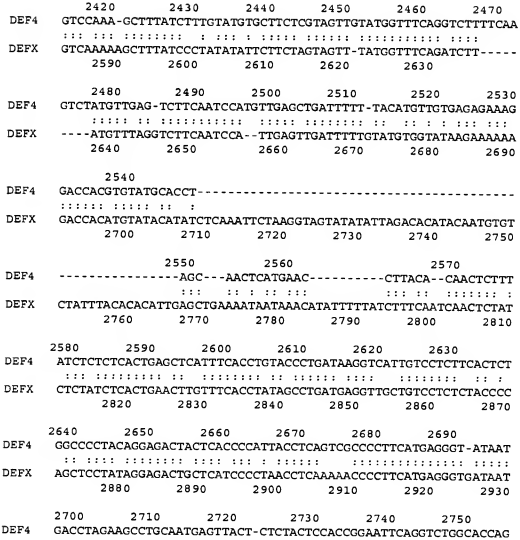

Figure 2(continued)

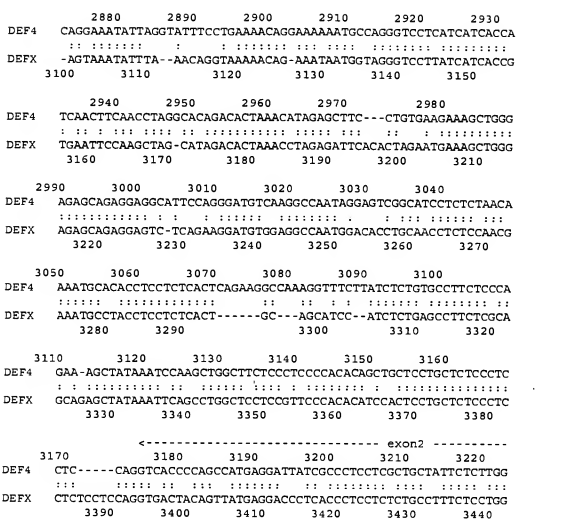

Figure 2(continued)

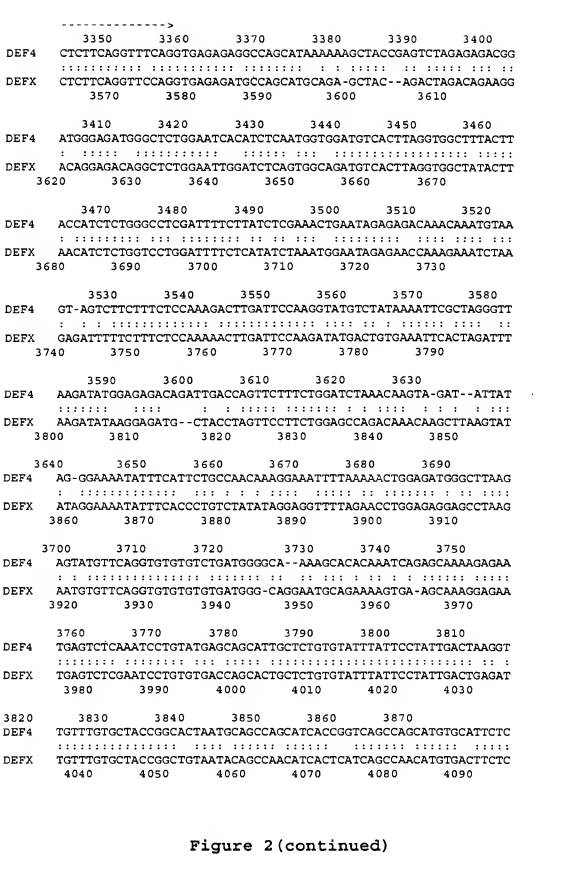

Figure 2(continued)

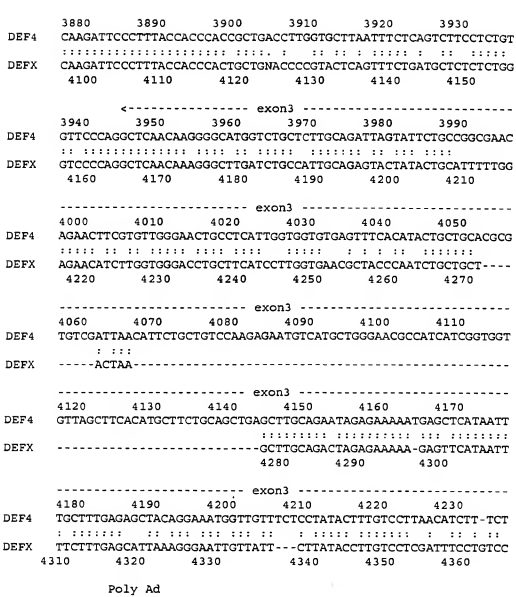

Figure 2(continued)

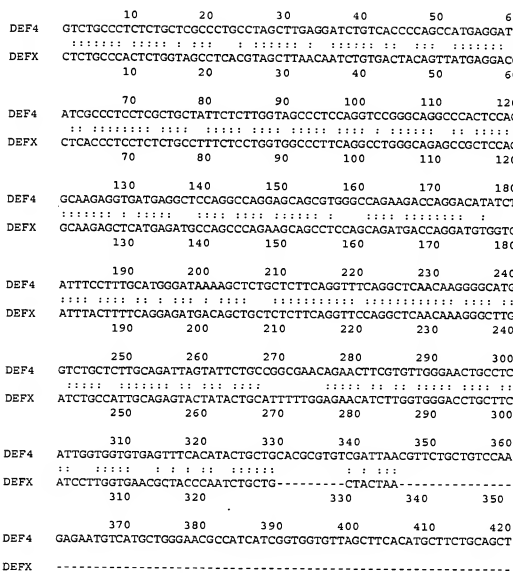

Figure 3

```
<----------------   Signal peptide  ---------------------><--
          5                  10                  15                  20
MetArgThrLeuThr LeuLeuSerAlaPhe LeuLeuValAlaLeu GlnAlaTrpAlaGlu

----------------------  Propiece  ---------------------------
          25                  30                  35                  40
ProLeuGlnAlaArg AlaHisGluMetPro AlaGlnLysGlnPro ProAlaAspAspGln

----------------------  Propiece  ---------------------------
          45                  50                  55                  60
AspValValIleTyr PheSerGlyAspAsp SerCysSerLeuGln ValProGlySerThr

--------><----------  Mature peptide  -------------------------
          65                  70                  75                  80
LysGlyLeuIleCys HisCysArgValLeu TyrCysIlePheGly GluHisLeuGlyGly

--------------------  Mature peptide  ----->
          85                  90                  94
ThrCysPheIleLeu GlyGluArgTyrPro IleCysCysTyr
```

Figure 4

```
                    SIGNAL                    PROPIECE
DEF4_HUMAN          MRIIALLAAILLVALQVRA  GPLQAR-------GDEAPGQ-EQRGPEDQDISISFAWDKSS
DEF5_HUMAN          MRTIAILAAILLVALQAQA  ESLQER-------ADEATTQ-KQSGEDNQDLAISFAGNGLS
DEF6_HUMAN          MRTLTILTAVLLVALQAKA  EPLQAEDDPLQAKAYEADAQ-EQRGANDQDFAVSFAEDASS
DEF1_HUMAN          MRTLAILAAILLVALQAQA  EPLQAR-------ADEVAAAPEQIAADIPEVVVSLAWDESL
DEFX                MRTLTLLSAFLLVALQAWA  EPLQAR-------AHEMPAQ-KQPPADDQDVVIYFSGDDSC
                    ** ...*.* ******  *    **           *     *       .  .  .

                     PROPIECE     Mature PEPTIDE
DEF4_HUMAN          ALQVSGSTRGM  VCSCRLVFCRRTELRVGNCLIGGVSFTYCCTRVD
DEF5_HUMAN          ALRTSGSQARA  TCYCRTGRCATRESLSGVCEISGRLYRLCCR---
DEF6_HUMAN          SLRALGSTRAF  TCHCRR-SCYSTEYSYGTCTVMGINHRFCCL---
DEF1_HUMAN          APKHPGSRKNM  ACYCRIPACIAGERRYGTCIYQGRLWAFCC----
DEFX                SLQVPGSTKGL  ICHCRVLYCIFGEHLGGTCFILGERYPICCY---
                    .  .   **     * **   *   *  * *   *      **
                                  ^ ^    ^          ^          ^^
```

Figure 5